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## CODA: shorthand for calling functions | HuBMAP | JHU-TMC V.1

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**We use this protocol and it's working**

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## Abstract

To downsample ndpi or svb images to 10x, 5x, and 1x tifs, use this function:

**create\_downsampled\_tif\_images**

or try Openslide in python

To calculate registration on the low resolution (1x) images

1. calculate the tissue area and background pixels using this function:

**calculate\_tissue\_ws**

2. calculate the registration transforms:

**calculate\_image\_registration**

To build a 3D tissue volume using semantic segmentation:

1. generate manual annotations in Aperio imagescope

2. apply the deep learning function to train a model and segment the high resolution (5x or 10x) images:

**train\_image\_segmentation**

To apply the registration to segmented images:

**apply\_image\_registration**

To build a 3D tissue matrix from registered, classified images:

**build\_tissue\_volume**

To build a 3D cell volume containing nuclear coordinates:

1. Build a mosaic image containing regions of many whole-slide images for cell detection optimization:

**make\_cell\_detection\_mosaic**

2. Manually annotate the mosaic image to get the 'ground-truth' number of cell nuclei:

**manual\_cell\_count**

3. Determine cell detection parameters using the manual annotations on the mosaic image:

**get\_nuclear\_detection\_parameters**

4. Deconvolve the high-resolution (5x or 10x) H&E images before applying the cell detection algorithm:

**deconvolve\_histological\_images**

5. Detect cells on the hematoxylin channel of the high-resolution images:

**cell\_detection**

6. Apply the registration to the cell coordinates:

**register\_cell\_coordinates**

7. Build a 3D cell coordinate matrix corresponding to the 3D tissue matrix:

**build\_cell\_volume**

